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RAW SEQUENCE LISTING

DATE: 03/22/2002

PATENT APPLICATION: US/09/966,955A

TIME: 14:45:54

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3 <110> APPLICANT: Perez-Villar, Juan J.
4   Chang, Han
5   Yang, Wen-Pin
6   Wu, Yuli
7   Whitney, Gena S.
8   Kanner, Steven B.
10 <120> TITLE OF INVENTION: Identification and Cloning of a Full-length Human
11   Clnk-related Gene, MIST (Mast Cell Immunoreceptor
12   Signal Transducer)
14 <130> FILE REFERENCE: 3053-4113US1
16 <140> CURRENT APPLICATION NUMBER: US/09/966,955A
17 <141> CURRENT FILING DATE: 2001-09-28
19 <150> PRIOR APPLICATION NUMBER: 60/237030
20 <151> PRIOR FILING DATE: 2000-09-29
22 <160> NUMBER OF SEQ ID NOS: 52
24 <170> SOFTWARE: PatentIn Ver. 2.1
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27 <211> LENGTH: 1851
28 <212> TYPE: DNA
29 <213> ORGANISM: HUMAN
31 <220> FEATURE:
32 <223> OTHER INFORMATION: HUMAN FULL-LENGTH MIST cDNA CLONE #8 - NUCLEIC
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38 ccagaggtcc aagatcctta caagggggcc agaaagggat gagctttctg aagaagcact 180
39 gatgtaaaat accaggaatt ttgacatcga agaagatttt tgtgatggca gctgggattt 240
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41 ctaaatgtgt gtgtcttcaa tggctgaatt gaagatccct ctaccgccgc aggtgccaag 360
42 aactatgaac aggcagggca atagaaagac aactaaagaa ggatccaacg atttgaaatt 420
43 ccagaacttc agtctgccaa aaaacagggtc atggcctcgc atcaatagtg ccacaggcca 480
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47 aactattttc aaggttgcaa tggacactcc ccttccgtta gacaccagga cctctatctc 720
48 cattggacag ccgacctgga acacacagac gaggttggaa agagtggaca aaccatttc 780
49 caaggacgtc agaagccaaa acattaaagg agatgcatcc gtaagaaaga acaagattcc 840
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51 gccggagagc agcaggccac ctttatctca gagacacacc tttccagaag tccagagaat 960
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53 taaccagagg aagcctgaat caactcatct gttagaaaac caaataactc aagagattcc 1080
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61 tgagaagttt gattcagtag aagacatcat cgaacactac aagaattttc ccattatact 1560
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65 gacaactttt ttaacttttg agaaaagaaa aacactctat aacagagagt ggaaaaatcac 1800
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74 <220> FEATURE:
75 <223> OTHER INFORMATION: HUMAN FULL-LENGTH MIST cDNA CLONE #8, TRANSLATED
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85 Lys Phe Gln Asn Phe Ser Leu Pro Lys Asn Arg Ser Trp Pro Arg Ile
86 35 40 45
88 Asn Ser Ala Thr Gly Gln Tyr Gln Arg Met Asn Lys Pro Leu Leu Asp
89 50 55 60
91 Trp Glu Arg Asn Phe Ala Ala Val Leu Asp Gly Ala Lys Gly His Ser
92 65 70 75 80
94 Asp Asp Asp Tyr Asp Asp Pro Glu Leu Arg Met Glu Glu Thr Trp Gln
95 85 90 95
97 Ser Ile Lys Ile Leu Pro Ala Arg Pro Ile Lys Glu Ser Glu Tyr Ala
98 100 105 110
100 Asp Thr His Tyr Phe Lys Val Ala Met Asp Thr Pro Leu Pro Leu Asp
101 115 120 125
103 Thr Arg Thr Ser Ile Ser Ile Gly Gln Pro Thr Trp Asn Thr Gln Thr
104 130 135 140
106 Arg Leu Glu Arg Val Asp Lys Pro Ile Ser Lys Asp Val Arg Ser Gln
107 145 150 155 160
109 Asn Ile Lys Gly Asp Ala Ser Val Arg Lys Asn Lys Ile Pro Leu Pro
110 165 170 175
112 Pro Pro Arg Pro Leu Ile Thr Leu Pro Lys Lys Tyr Gln Pro Leu Pro
113 180 185 190
115 Pro Glu Pro Glu Ser Ser Arg Pro Pro Leu Ser Gln Arg His Thr Phe
116 195 200 205
118 Pro Glu Val Gln Arg Met Pro Ser Gln Ile Ser Leu Arg Asp Leu Ser
119 210 215 220
121 Glu Val Leu Glu Ala Glu Lys Val Pro His Asn Gln Arg Lys Pro Glu

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128          260          265          270
130 Asp His Arg Gly Gly Met Gln Pro Cys Ser Pro Gln Arg Cys Gln Pro
131          275          280          285
133 Pro Ala Ser Cys Ser Pro His Glu Asn Ile Leu Pro Tyr Lys Tyr Thr
134          290          295          300
136 Ser Trp Arg Pro Pro Phe Pro Lys Arg Ser Asp Arg Lys Asp Val Gln
137 305          310          315          320
139 His Asn Glu Trp Tyr Ile Gly Glu Tyr Ser Arg Gln Ala Val Glu Glu
140          325          330          335
142 Ala Phe Met Lys Glu Asn Lys Asp Gly Ser Phe Leu Val Arg Asp Cys
143          340          345          350
145 Ser Thr Lys Ser Lys Glu Glu Pro Tyr Val Leu Ala Val Phe Tyr Glu
146          355          360          365
148 Asn Lys Val Tyr Asn Val Lys Ile Arg Phe Leu Glu Arg Asn Gln Gln
149          370          375          380
151 Phe Ala Leu Gly Thr Gly Leu Arg Gly Asp Glu Lys Phe Asp Ser Val
152 385          390          395          400
154 Glu Asp Ile Ile Glu His Tyr Lys Asn Phe Pro Ile Ile Leu Ile Asp
155          405          410          415
157 Gly Lys Asp Lys Thr Gly Val His Arg Lys Gln Cys His Leu Thr Gln
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165 <211> LENGTH: 2335
166 <212> TYPE: DNA
167 <213> ORGANISM: HUMAN
169 <220> FEATURE:
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176 actaatttcc agtgcâccaa ggtctctgca ctgâcgcâcc tcctcacagg agacggacac 180
177 ctcagcctag atcccttggg gctctccacg ctgttcaggc tgaattgaag atccctctta 240
178 cccgccagggt gccâagaact atgaacaggc agggcaatag aaagacaact aaagaaggat 300
179 ccaacgattt gaaattccag aacttcagtc tgccââââââ caggtcatgg cctcgcacatca 360
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181 ttgctgcagt cctggatgga gcaâââaggcc acagtgtatga tgactatgat gaccctgagc 480
182 ttcggatgga agagacatgg cagtcgatta aaattttacc agcccgccct atâââaggâat 540
183 ctgaatatgc agatacacac tatttcaagg ttgcaatgga cactccctt ccgttagaca 600
184 ccaggacctc tatctccatt ggacagccga cctggaacac acagacgagg ttggââââgag 660
185 tggacââââc catttccââg gacgtcâgââ gccââââââc taaaggagat gcatccgtaa 720
186 gââââââââ gattccttta ccacctcctc ggâcctctcat aacacttccg aâgââgâtâc 780
187 aâcccttgcc ccctgâgâccg gagâgâcâgââ ggccâcctt atctcâgâgâ câcâccttâc 840

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190 atactcaaga gattccactt gccattagca gttcttcatt cagacaagc aaccacagt 1020
191 tgcaaaacag agatcataga ggaggcagtc agccctgttc tcctcagaga tgccagcctc 1080
192 cagccagctg cagccctcac gaaaatatac tgccctataa atacacaagc tggagaccac 1140
193 ctttcccaa aaggtctgat agaaaggatg tccagcaca tgaatggtac attggagaat 1200
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195 tccgagattg ttccacaaaa tccaaggaag agccctatgt tttggctgtg ttttatgaga 1320
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197 caggactcag aggagatgag aagtttgatt cagtagaaga catcatcgaa cactacaaga 1440
198 attttcccat tatactaatt gatgggaaa ataaaaactgg ggtccacagg aaacagtgtc 1500
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202 gagagtggaa aatcactcac ggttttgaat gttcaaacca cagagaaaat atttataaca 1740
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205 gctcatgata caggcgagca gcaaagggca ccagaagctg ttgcttaa at gtttgcagtc 1920
206 agtgcaagac aagtctatgg gaaattccca aatctgtgct ctttacagga cactgcgctg 1980
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209 tggacagatc acgaggtcag gagatcaaga ccactctggc taacatggtg aaaccccatg 2160
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211 tcgggagggt gaggcaggag aatggtgtga acccgggagg cggagcttgc agtgagccga 2280
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215 <210> SEQ ID NO: 4

216 <211> LENGTH: 428

217 <212> TYPE: PRT

218 <213> ORGANISM: HUMAN

220 <220> FEATURE:

221 <223> OTHER INFORMATION: HUMAN MIST SPLICE VARIANT CLONE #7, AMINO ACID
 222 SEQUENCE

224 <400> SEQUENCE: 4

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229             20             25             30
231 Ile Asn Ser Ala Thr Gly Gln Tyr Gln Arg Met Asn Lys Pro Leu Leu
232             35             40             45
234 Asp Trp Glu Arg Asn Phe Ala Ala Val Leu Asp Gly Ala Lys Gly His
235             50             55             60
237 Ser Asp Asp Asp Tyr Asp Pro Glu Leu Arg Met Glu Glu Thr Trp
238             65             70             75             80
240 Gln Ser Ile Lys Ile Leu Pro Ala Arg Pro Ile Lys Glu Ser Glu Tyr
241             85             90             95
243 Ala Asp Thr His Tyr Phe Lys Val Ala Met Asp Thr Pro Leu Pro Leu
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256      165      170      175
258 Pro Pro Glu Pro Glu Ser Ser Arg Pro Pro Leu Ser Gln Arg His Thr
259      180      185      190
261 Phe Pro Glu Val Gln Arg Met Pro Ser Gln Ile Ser Leu Arg Asp Leu
262      195      200      205
264 Ser Glu Val Leu Glu Ala Glu Lys Val Pro His Asn Gln Arg Lys Pro
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267 Glu Ser Thr His Leu Leu Glu Asn Gln Asn Thr Gln Glu Ile Pro Leu
268 225      230      235      240
270 Ala Ile Ser Ser Ser Ser Phe Thr Thr Ser Asn His Ser Val Gln Asn
271      245      250      255
273 Arg Asp His Arg Gly Gly Met Gln Pro Cys Ser Pro Gln Arg Cys Gln
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276 Pro Pro Ala Ser Cys Ser Pro His Glu Asn Ile Leu Pro Tyr Lys Tyr
277      275      280      285
279 Thr Ser Trp Arg Pro Pro Phe Pro Lys Arg Ser Asp Arg Lys Asp Val
280      290      295      300
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283 305      310      315      320
285 Glu Ala Phe Met Lys Glu Asn Lys Asp Gly Ser Phe Leu Val Arg Asp
286      325      330      335
288 Cys Ser Thr Lys Ser Lys Glu Glu Pro Tyr Val Leu Ala Val Phe Tyr
289      340      345      350
291 Glu Asn Lys Val Tyr Asn Val Lys Ile Arg Phe Leu Glu Arg Asn Gln
292      355      360      365
294 Gln Phe Ala Leu Gly Thr Gly Leu Arg Gly Asp Glu Lys Phe Asp Ser
295      370      375      380
297 Val Glu Asp Ile Ile Glu His Tyr Lys Asn Phe Pro Ile Ile Leu Ile
298 385      390      395      400
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312 <220> FEATURE:
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VERIFICATION SUMMARY

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